

FIG 1

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Reconstitution of lysis with anti KIR2D mAb on C1R
Cw4 target at effector /target ratio of 4/1

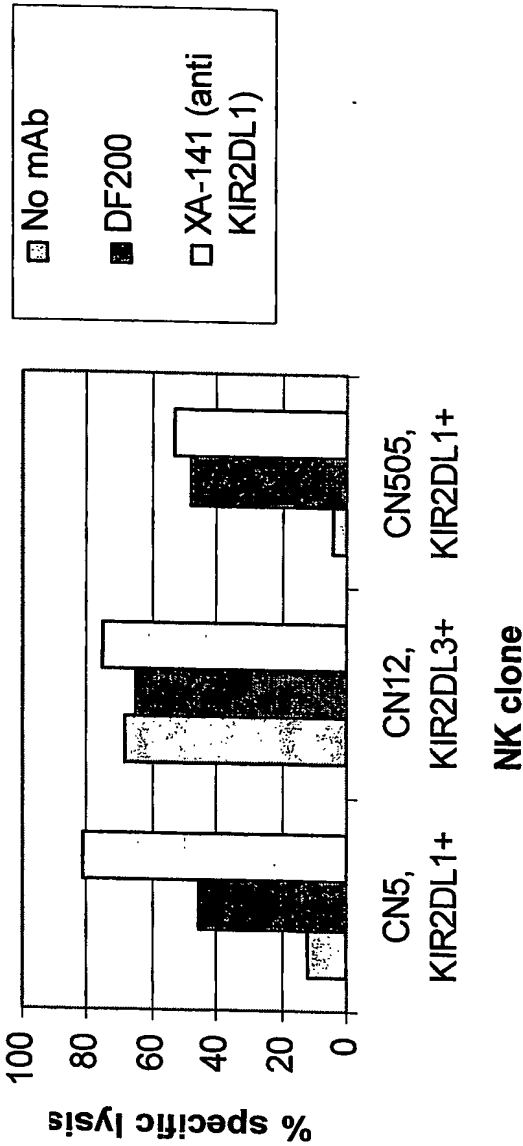


FIG 2

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FIG 3

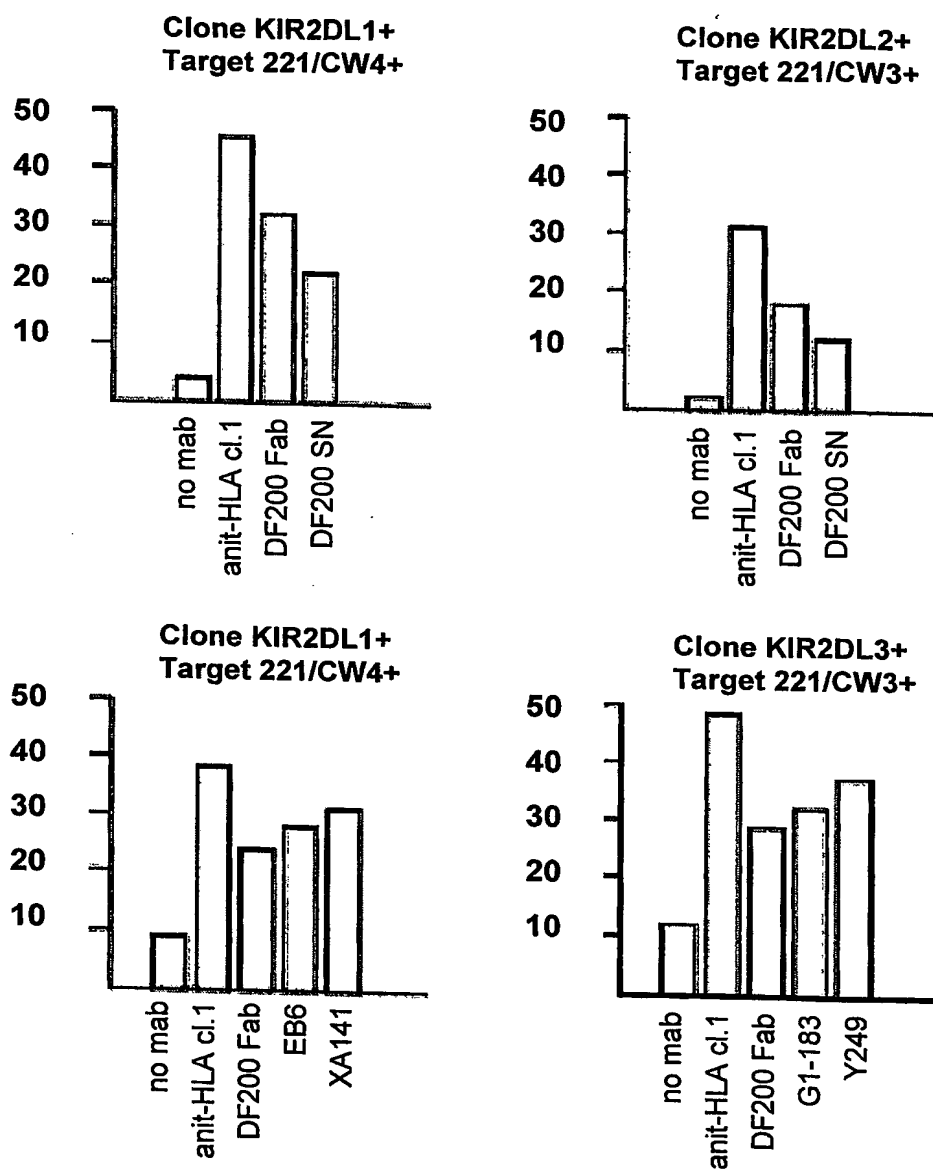
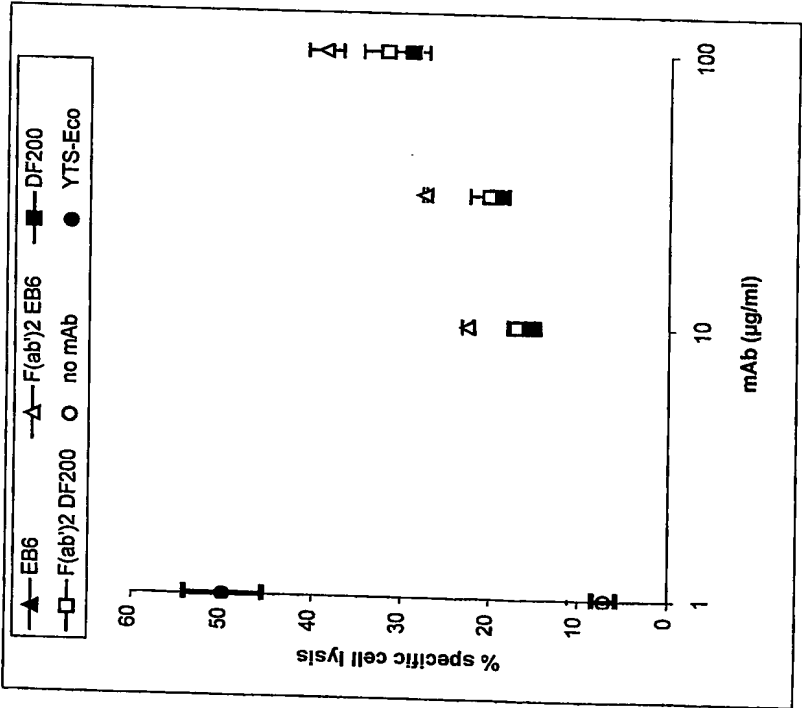


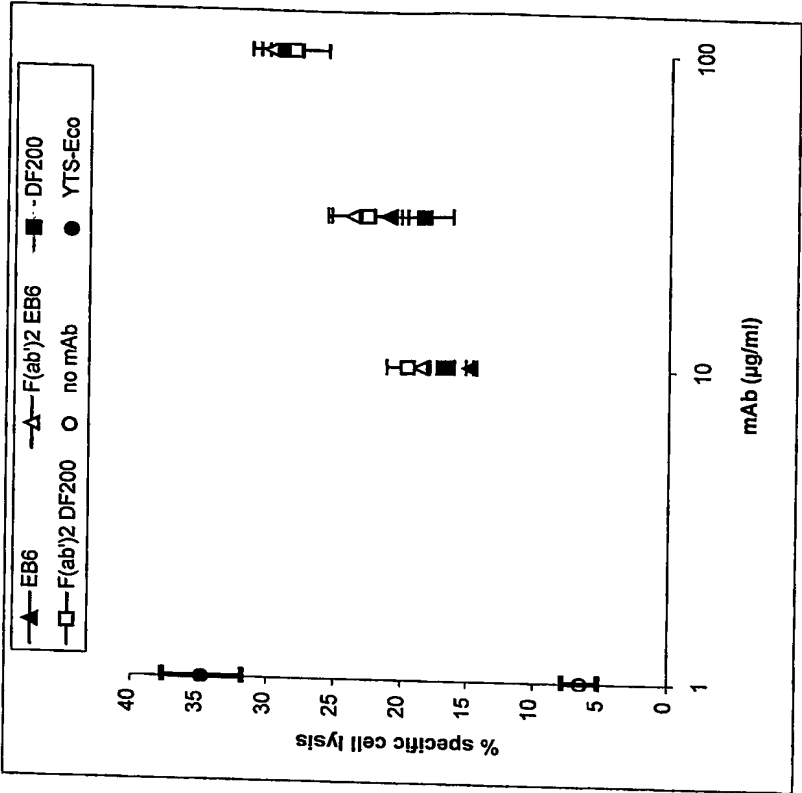
FIG 4

Target cell: FIG 4A : 721.221-cw4



E/T ratio= 1

FIG 4B : TUBO



E/T ratio= 2

FIG 5

FIG 5B : mAb: 10µg/ml

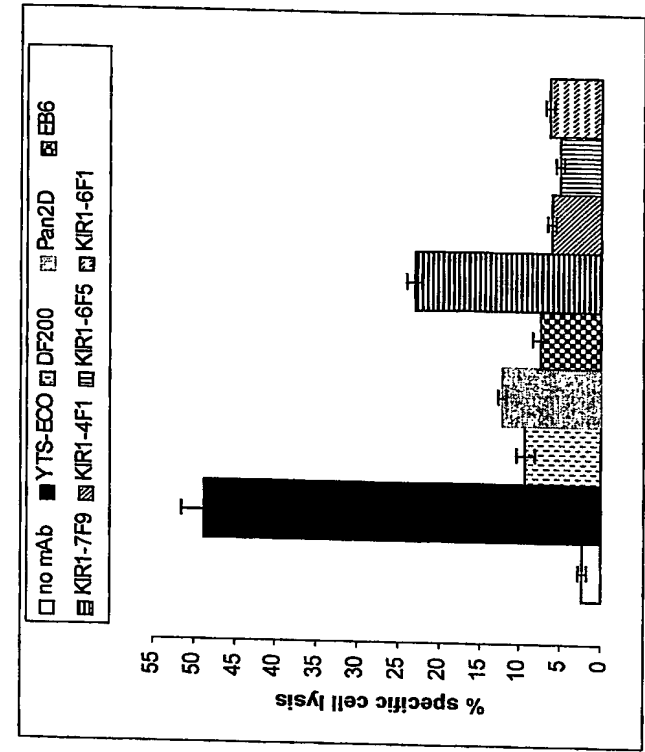
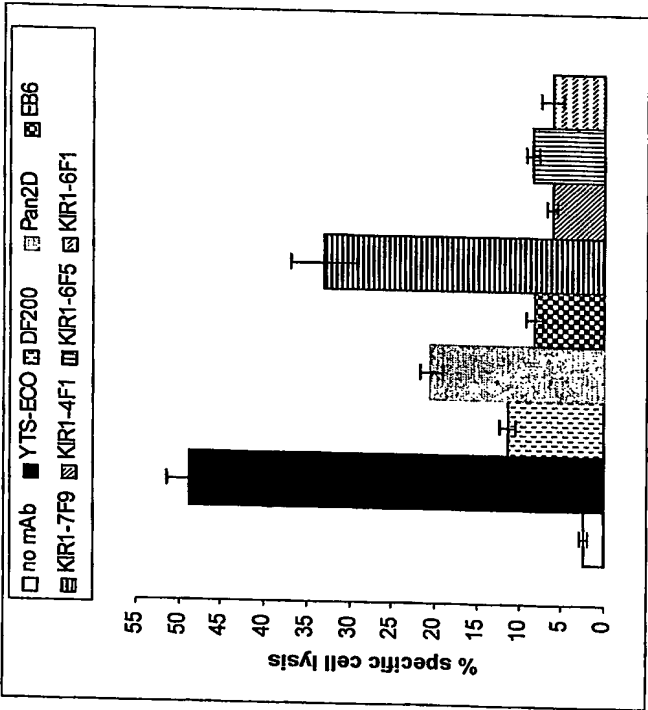


FIG 5A : mAb: 30µg/ml



E/T ratio= 1

Rest Available Copy

FIG 6

FIG 6B : mAb: 10µg/ml

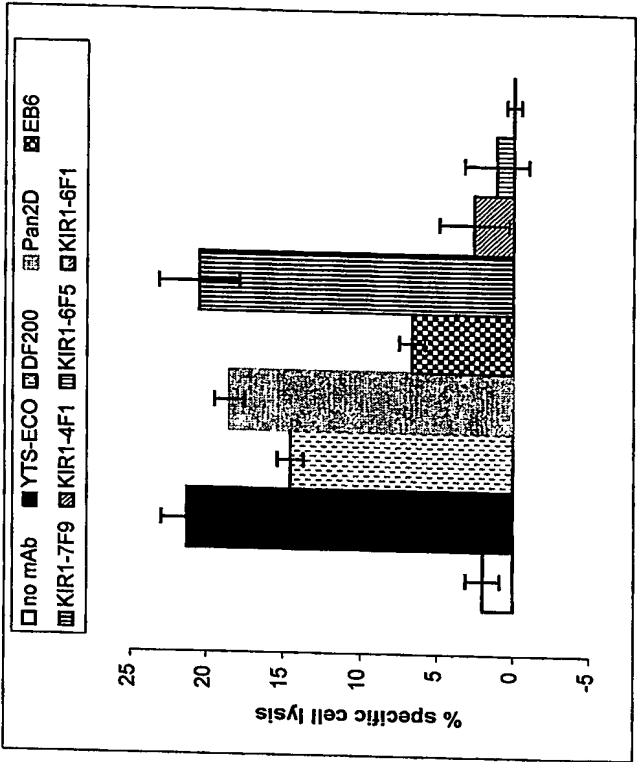
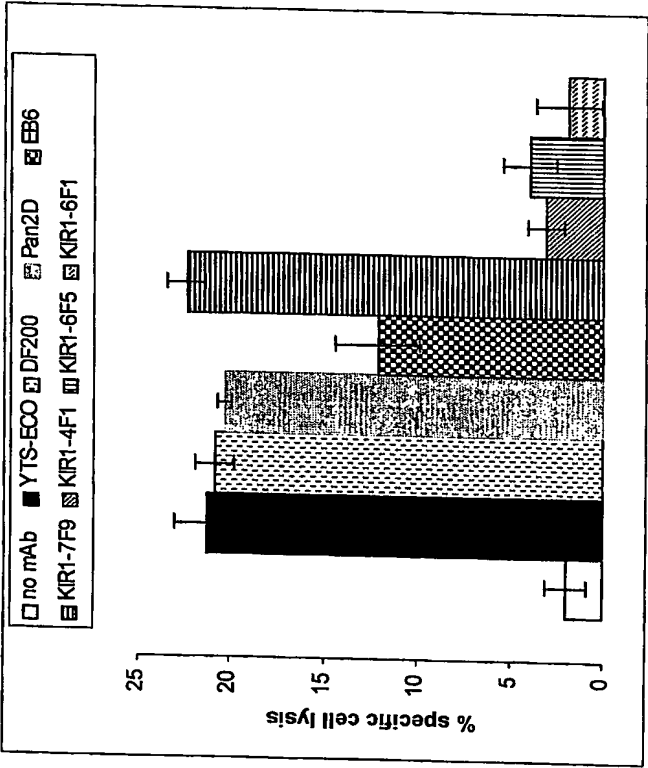


FIG 6A: mAb: 30µg/ml



E/T ratio= 2

Best Available Copy

FIG 7

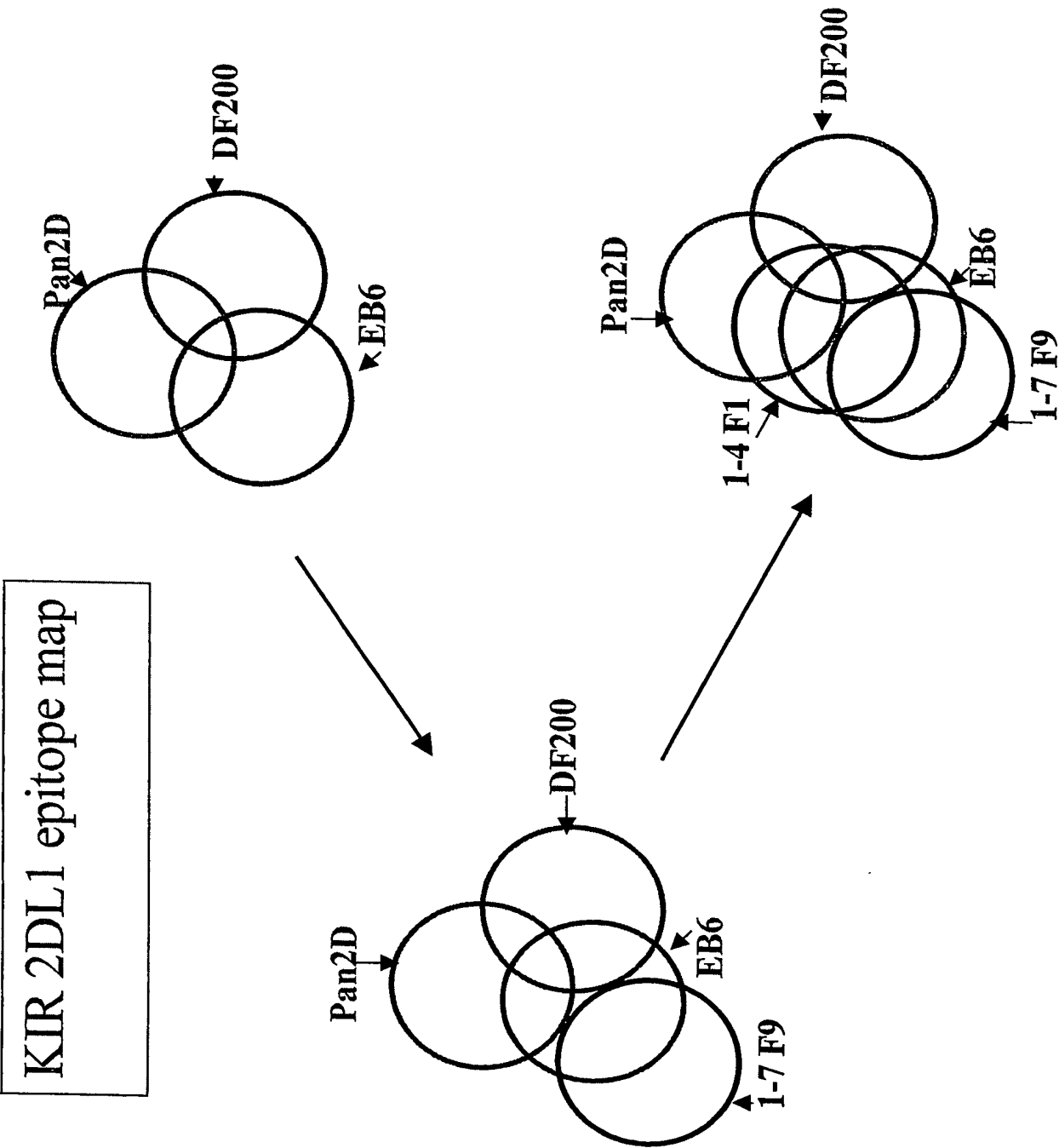
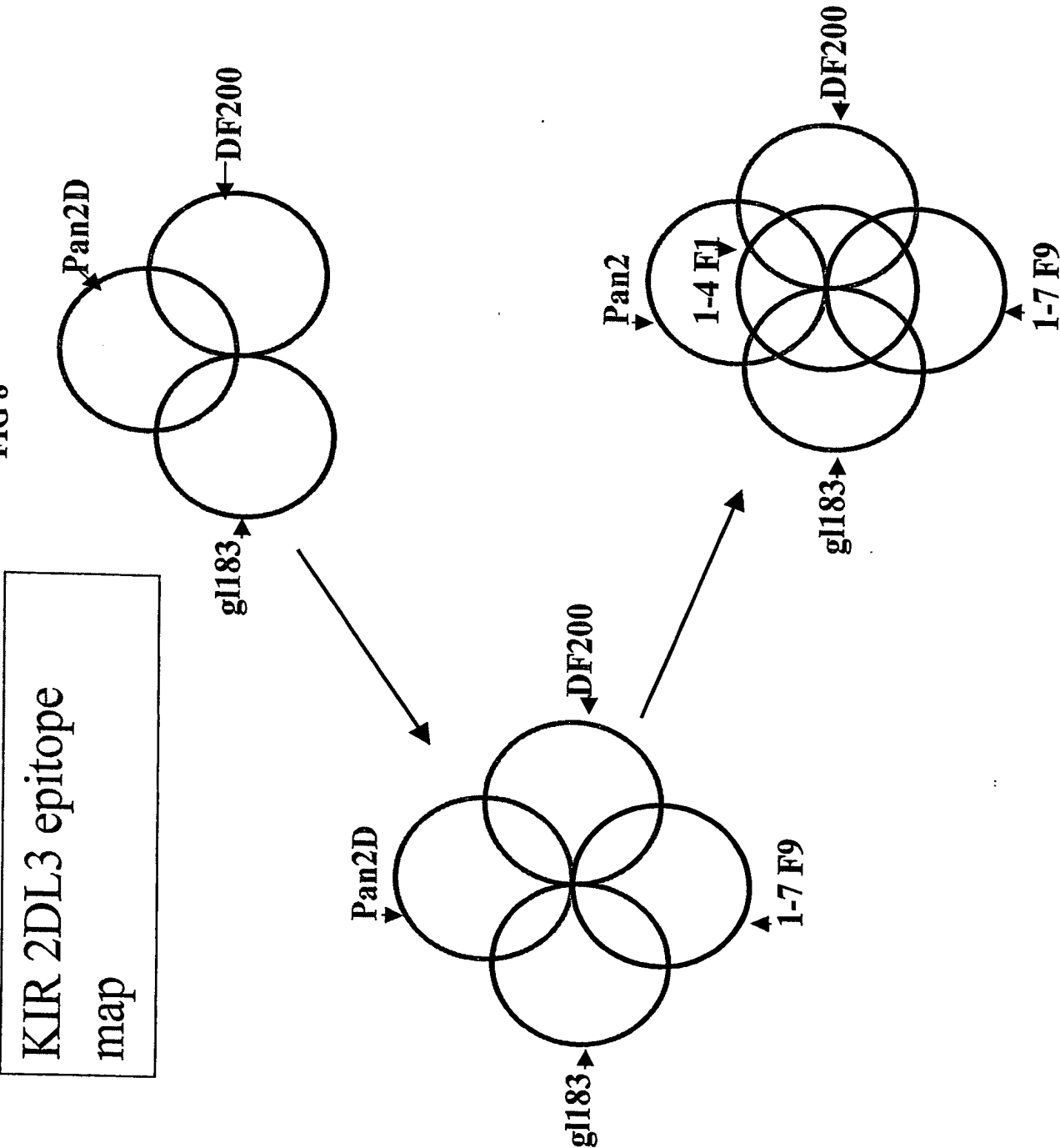


FIG 8



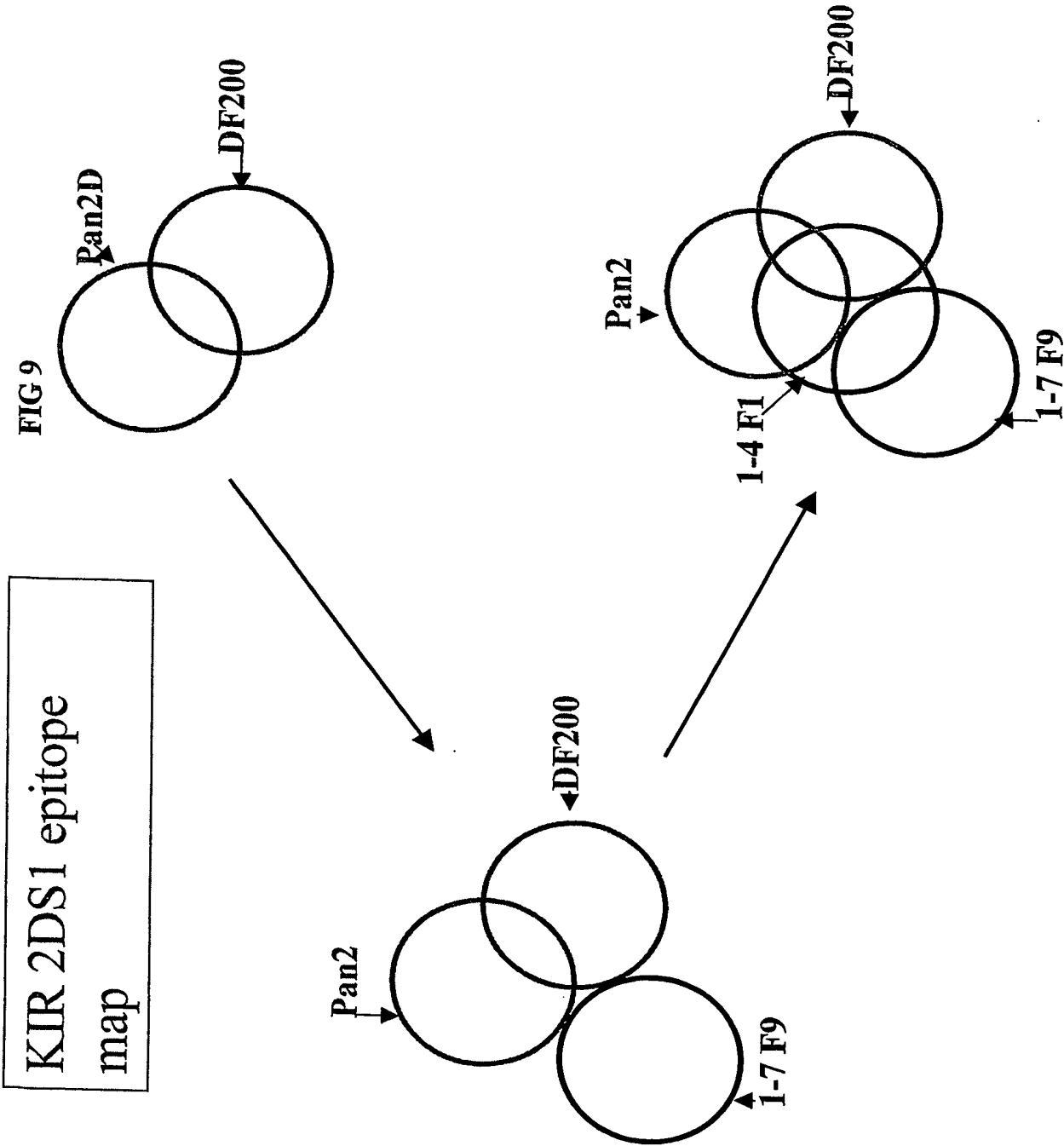
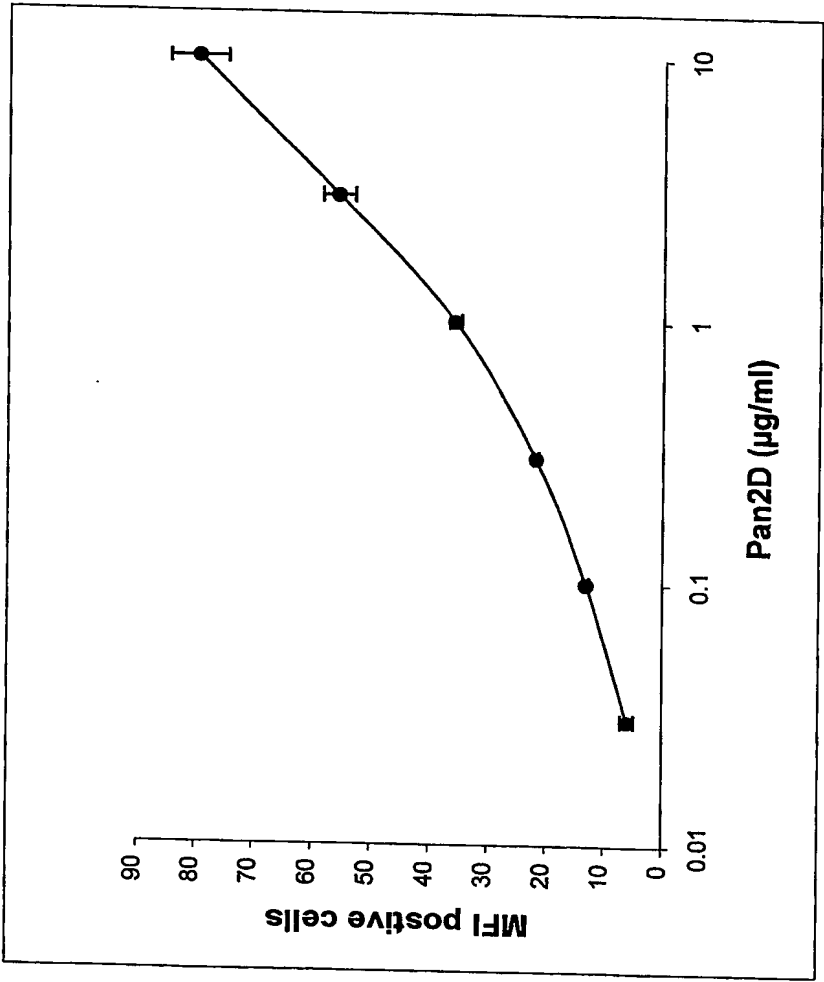


FIG 10



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FIG 11

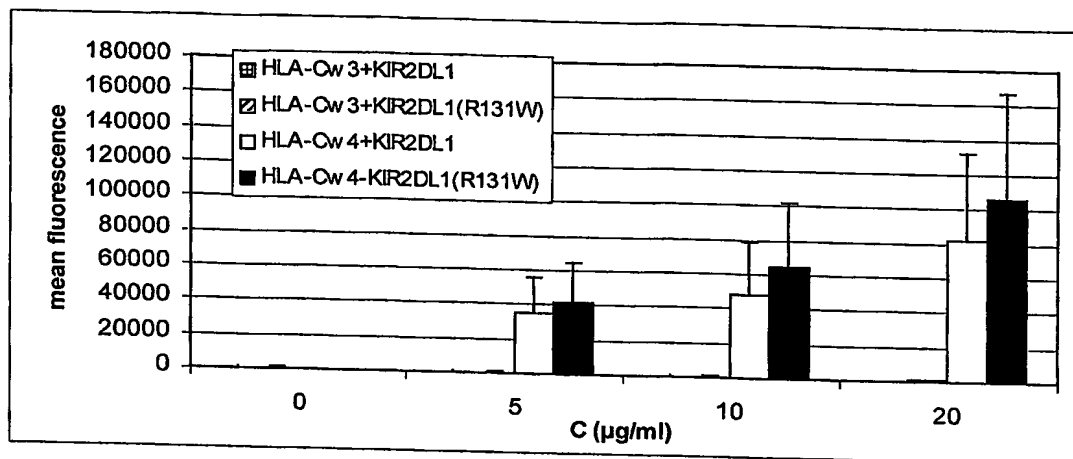
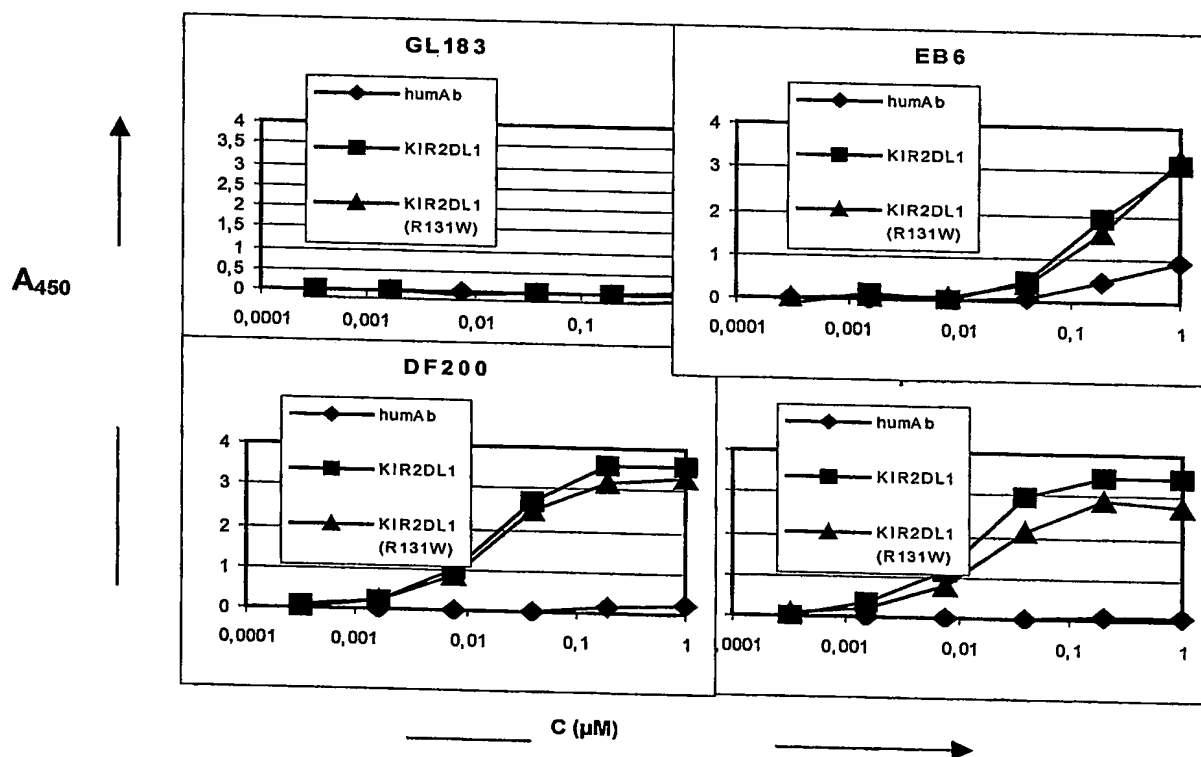
FIG 11A KIR2DL1(R131W)-hFc**FIG 11B**

FIG 12

Anti-KIR light variable regions

DF-200 light variable	(1)	<u>M</u> - - <u>E</u> <u>S</u> <u>O</u> <u>T</u> <u>L</u> <u>V</u> <u>F</u> <u>S</u> <u>I</u> <u>L</u> <u>L</u> <u>M</u> <u>I</u> <u>G</u> <u>A</u> <u>D</u> <u>G</u> <u>N</u> <u>I</u> <u>V</u> <u>T</u> <u>O</u> <u>S</u> <u>P</u> <u>K</u> <u>S</u> <u>M</u> <u>S</u> <u>M</u> <u>S</u> <u>V</u> <u>G</u> <u>E</u> <u>R</u> <u>V</u> <u>T</u> <u>T</u> <u>C</u> <u>K</u> <u>A</u> <u>S</u> <u>E</u> <u>N</u>	50
PAN2D-Light-variable	(1)	<u>M</u> <u>D</u> <u>F</u> <u>Q</u> <u>V</u> <u>I</u> <u>F</u> <u>S</u> <u>F</u> <u>L</u> <u>I</u> <u>S</u> <u>A</u> <u>M</u> <u>I</u> <u>M</u> <u>S</u> <u>R</u> <u>G</u> <u>I</u> <u>V</u> <u>E</u> <u>T</u> <u>O</u> <u>S</u> <u>P</u> <u>A</u> <u>S</u> <u>M</u> <u>S</u> <u>A</u> <u>S</u> <u>G</u> <u>E</u> <u>R</u> <u>V</u> <u>T</u> <u>T</u> <u>C</u> <u>T</u> <u>A</u> <u>S</u> <u>S</u>	
Consensus	(1)	Q F I I L A G N I V I T Q S P S M S S I G E R V T I T C A S	100
DF-200 light variable	(49)	<u>V</u> <u>V</u> <u>T</u> - <u>V</u> <u>S</u> <u>W</u> <u>Y</u> <u>Q</u> <u>Q</u> <u>K</u> <u>P</u> <u>E</u> <u>O</u> <u>S</u> <u>P</u> <u>K</u> <u>L</u> <u>I</u> <u>I</u> <u>G</u> <u>A</u> <u>S</u> <u>N</u> <u>R</u> <u>Y</u> <u>T</u> <u>G</u> <u>V</u> <u>P</u> <u>D</u> <u>R</u> <u>F</u> <u>T</u> <u>G</u> <u>S</u> <u>G</u> <u>S</u> <u>A</u> <u>T</u> <u>D</u> <u>E</u> <u>L</u> <u>T</u> <u>I</u> <u>S</u>	100
PAN2D-Light-variable	(51)	<u>V</u> <u>S</u> <u>S</u> <u>T</u> <u>L</u> <u>Y</u> <u>W</u> <u>Y</u> <u>Q</u> <u>Q</u> <u>K</u> <u>P</u> <u>G</u> <u>S</u> <u>S</u> <u>P</u> <u>K</u> <u>L</u> <u>I</u> <u>I</u> <u>G</u> <u>A</u> <u>S</u> <u>N</u> <u>R</u> <u>Y</u> <u>T</u> <u>G</u> <u>V</u> <u>P</u> <u>D</u> <u>R</u> <u>F</u> <u>T</u> <u>G</u> <u>S</u> <u>G</u> <u>S</u> <u>A</u> <u>T</u> <u>D</u> <u>E</u> <u>L</u> <u>T</u> <u>I</u> <u>S</u>	
Consensus	(51)	V S Y L W Y Q Q K P S P K L I Y S N S G V P R F S G S G S A T F S L T I S S	131
DF-200 light variable	(98)	<u>Q</u> <u>A</u> <u>E</u> <u>D</u> <u>L</u> <u>A</u> <u>D</u> <u>V</u> <u>H</u> <u>C</u> <u>G</u> <u>Q</u> <u>G</u> <u>S</u> <u>Y</u> <u>P</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>T</u> <u>K</u> <u>L</u> <u>E</u> <u>I</u> <u>K</u> <u>R</u>	
PAN2D-Light-variable	(101)	<u>M</u> <u>E</u> <u>A</u> <u>E</u> <u>D</u> <u>A</u> <u>A</u> <u>T</u> <u>V</u> <u>C</u> <u>H</u> <u>Q</u> <u>Y</u> <u>E</u> <u>R</u> <u>S</u> <u>P</u> <u>P</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>T</u> <u>K</u> <u>L</u> <u>E</u> <u>I</u> <u>K</u> <u>R</u>	
Consensus	(101)	M A E D A Y H C Q Y E R S P P T F G G T K L E I K R	

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

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CDR's from the anti-KIR light variable regions

CDR-L1 from clones PAN-2D and DF-200	
Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu.Length: 10-17 aa	
Start: approximately 24 aa from the beginning of secreted protein	
DF-200 light variable (44) <u>K</u> <u>A</u> <u>S</u> <u>E</u> <u>N</u> <u>V</u> <u>V</u> <u>T</u> - <u>Y</u> <u>S</u>	
PAN2D-Light-variable (46) <u>T</u> <u>A</u> <u>S</u> <u>S</u> <u>S</u> <u>V</u> <u>S</u> <u>S</u> <u>S</u> <u>Y</u> <u>P</u> <u>T</u>	
Consensus AS V S Y L	
CDR-L3 from clones PAN-2D and DF-200	
Residues before: Cys	
Residues after: Phe-Gly-XXX-Gly	
Length: 7-11 aa	
Start: approximately 33 aa after the end of CDR-L2	
DF-200 light variable (109) <u>G</u> <u>Q</u> <u>G</u> <u>S</u> <u>Y</u> <u>P</u> <u>T</u>	
PAN2D-Light-variable (112) <u>H</u> <u>Q</u> <u>Y</u> <u>E</u> <u>R</u> <u>S</u> <u>P</u> <u>P</u> <u>T</u>	
Consensus Q H P T	
CDR-L2 from clones PAN-2D and DF-200	
Residues before: Generally Ile-Tyr	
Length: 7 aa	
Start: approximately 16 aa after the end of CDR-L1	
DF-200 light variable (70) <u>G</u> <u>A</u> <u>S</u> <u>N</u> <u>R</u> <u>Y</u> <u>T</u>	
PAN2D-Light-variable (73) <u>S</u> <u>T</u> <u>S</u> <u>N</u> <u>L</u> <u>A</u> <u>S</u>	
Consensus S N S	

FIG 13

>DF-200\|VH\immature-PROT
MAVLGLLFLCLVTFPSCVLS
QVLEQSGPGLVQPSQSLSTCTVSGFSFTPYGVHWVRQSPGKGLEWLGVIWSGGNTDYNAAFISRLSINKDNSKSQVFFKMNSLQVND
TAIYYCARNPRPGNYPYGMDYWGQGTSTVTVSS

Anti-KIR heavy variable regions (immature Fabs)

Sequences including CDR regions in heavy variable regions

<p>CDR-H1 from clone DF-200 Residues before: Cys-XXX-XXX-XXX Residues after: Trp. Generally Trp-Val or Trp-Ile Length: 10-14 aa Start: Approximately 22-26 aa from the beginning of the secreted protein</p> <p>GFSFTPYGVH</p>	<p>CDR-H2 from clone DF-200 Residues before: Leu-Glu-Trp-Ile-Gly but other variations possible Residues after: Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala Length: 16-20 aa Start: Approximately 15 aa after the end of CDR-H1</p> <p>VIWSGGNTDYNAAFIS</p>
<p>CDR-H3 from clones 4G1, 5D5 and 6C12 Residues before: Cys-XXX-XXX (Typically Cys-Ala-Arg) Residues after: Trp-Gly-XXX-Gly Length: 3-25 aa Start: Approximately 33 after the end of CDR-H2</p> <p>NPRPGNYPYGMDY</p>	

The secreted, mature VH starts at:
Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown) continues